

SCORE Search Results Details for Application 10764186 and Search Result 20070816_164306_us-10-764-186-1.rng.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

10/764,186

This page gives you Search Results detail for the Application 10764186 and Search Result 20070816_164306_us-10-764-186-1.rng.

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OM nucleic - nucleic search, using sw model

Run on: August 19, 2007, 16:31:34 ; Search time 213 Seconds
(without alignments)
731.716 Million cell updates/sec

Title: US-10-764-186-1
Perfect score: 21
Sequence: 1 ttgcaaattcttttctctggtg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	21	10	ADK69887	Adk69887 Borrelia
2	21	100.0	226	2	AAQ20446	Aaq20446 B.burgdor
3	21	100.0	381	2	AAQ41495	Aaq41495 Flagellin
4	21	100.0	404	2	AAQ32998	Aaq32998 DNA encod
5	21	100.0	747	2	AAQ41493	Aaq41493 Flagellin
6	21	100.0	1011	2	AAQ20720	Aaq20720 B.burgdor
7	21	100.0	1011	2	AAQ90744	Aaq90744 B. burgdo
8	21	100.0	1011	6	ABK47872	Abk47872 DNA encod
9	21	100.0	1011	6	ABK47871	Abk47871 DNA encod
10	21	100.0	1131	2	AAQ41494	Aaq41494 CKS-410 f
11	21	100.0	1141	2	AAQ90737	Aaq90737 B31 outer
12	21	100.0	1141	6	ABK47864	Abk47864 Borrelia
13	21	100.0	1180	2	AAQ90735	Aaq90735 B31 outer
14	21	100.0	1180	6	ABK47862	Abk47862 Borrelia
15	21	100.0	1324	2	AAQ90738	Aaq90738 B31 outer
16	21	100.0	1324	6	ABK47865	Abk47865 Borrelia
17	21	100.0	1363	2	AAQ90736	Aaq90736 B31 outer
18	21	100.0	1363	6	ABK47863	Abk47863 Borrelia
19	21	100.0	1497	2	AAQ41492	Aaq41492 CKS-776 f
20	21	100.0	1507	2	AAQ27078	Aaq27078 Fla gene
21	21	100.0	1762	2	AAQ90739	Aaq90739 B31 Osp-A
22	21	100.0	1765	6	ABK47866	Abk47866 Borrelia
23	21	100.0	110000	2	AAX20248_07	Continuation (8 of
24	19.4	92.4	226	2	AAQ20447	Aaq20447 B.burgdor
25	19.4	92.4	226	2	AAQ20448	Aaq20448 B.burgdor
26	19.4	92.4	1011	6	ABK47821	Abk47821 Borrelia
27	18.4	87.6	930	13	ADS47133	Ads47133 Bacterial
28	18.4	87.6	83946	6	ABQ88101	Abq88101 Human ost
29	18.4	87.6	83946	12	ADQ17978	Adq17978 Human sof
c 30	18.4	87.6	149671	6	ABK84797	Abk84797 Human cDN
c 31	18.4	87.6	149671	9	ADB70361	Adb70361 Moesin cD
c 32	18.4	87.6	149671	12	ADJ37140	Adj37140 Human mal
33	18	85.7	1276	4	AAS12520	Aas12520 Gene #13
34	18	85.7	1276	10	ABQ77257	Abq77257 Human ser
35	18	85.7	2138	13	ADR07469	Adr07469 Full leng
36	18	85.7	4750	12	ADQ19282	Adq19282 Human sof
37	18	85.7	4750	13	ADR89531	Adr89531 Apoptosis
38	18	85.7	4874	14	ADZ13314	Adz13314 Human can
39	18	85.7	4887	12	ADQ23550	Adq23550 Human sof
40	18	85.7	5008	13	ADR06934	Adr06934 Full leng
41	18	85.7	89625	11	ACN45194	Acn45194 Human gen
42	18	85.7	91279	14	ADZ13313	Adz13313 Human can
43	17.8	84.8	226	2	AAQ20449	Aaq20449 B.burgdor
44	17.8	84.8	510	6	ABK92507	Abk92507 Human pro
45	17.8	84.8	1011	6	ABK47820	Abk47820 Borrelia

ALIGNMENTS

DT 25-MAR-2003 (revised)
 DT 20-AUG-1993 (first entry)
 XX
 DE Flagellin (amino acids 64-311).
 XX
 KW CMP-KDO synthetase; pB776; pB410; capture; immunodot; assay;
 KW Treponema pallidum; syphilis;
 KW CTP: CMP-3-deoxy-manno-octulosonate cytidyl transferase; ss.
 XX
 OS Borrelia burgdorferi.
 XX
 PN WO9308208-A1.
 XX
 PD 29-APR-1993.
 XX
 PF 21-OCT-1992; 92WO-US009199.
 XX
 PR 21-OCT-1991; 91US-00779704.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Robinson JM, Pilot-Matias TJ, Hunt JC;
 XX
 DR WPI; 1993-152418/18.
 DR P-PSDB; AAR36698.
 XX
 PT Synthetic polypeptide immuno-reactive with Borrelia Burgdorferi
 PT antibodies - for diagnosis of Lyme disease.
 XX
 PS Claim 11; Page 42; 76pp; English.
 XX
 CC Expression vector pB776 encodes fusion protein CKS-776, consisting of 239
 CC amino acids of CKS, 11 amino acids contributed by linker DNA sequences,
 CC and amino acids 64 to 311 of B. burgdorferi flagellin. The recombinant
 CC fusion proteins p776 and p410 are differentiating polypeptides which can
 CC be used in capture assays and immunodot assays for the detection of B.
 CC burgdorferi infection such as in Lyme disease, without false positives
 CC due to Treponema pallidum infection such as in patients with syphilis.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 747 BP; 274 A; 128 C; 149 G; 196 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 747;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCAAATCTTTTCTCTGGTG 21
 |||||
 Db 392 TTGCAAATCTTTTCTCTGGTG 412

RESULT 6

AAQ20720

ID AAQ20720 standard; DNA; 1011 BP.

XX

AC AAQ20720;

XX

DT 25-MAR-2003 (revised)

DT 15-APR-1992 (first entry)

XX

DE B.burgdorferi flagellin gene.

```

XX
KW    tick-borne spirochaete; Lyme disease; polymerase chain reaction; PCR; ss.
XX
OS    Borrelia burgdorferi.
XX
FH    Key                Location/Qualifiers
FT    misc_feature       390. .712
FT                                /*tag= b
FT                                /note= "region of relative non-homology to B.hermsii"
FT    misc_feature       492. .516
FT                                /*tag= c
FT                                /note= "primer for amplifying B.burgdorferi DNA"
FT    misc_feature       594. .642
FT                                /*tag= a
FT                                /label= Probe
FT                                /note= "specific for B.burgdorferi B31 group"
FT    misc_feature       743. .767
FT                                /*tag= d
FT                                /note= "primer for amplifying B.burgdorferi DNA"
XX
PN    WO9119814-A.
XX
PD    26-DEC-1991.
XX
PF    15-JUN-1990;      90US-00538957.
XX
PR    15-JUN-1990;      90US-00538957.
PR    25-APR-1991;      91US-00691188.
XX
PA    (BAXT ) BAXTER DIAGNOSTICS INC.
XX
PI    Picken RN,  Ammons HC;
XX
DR    WPI; 1992-024430/03.
XX
PT    New DNA primers useful in diagnosis of Lyme's disease - comprise
PT    complementary strand specificity flanking Borrelia burgdorferi sequence.
XX
PS    Disclosure; Fig 1; 47pp; English.
XX
CC    Comparison of this sequence from B.burgdorferi with the flagellin gene of
CC    B.hermsii (see AAQ20721) revealed a region of relative non-homology. This
CC    region provides the basis for constructing primers and probes which are
CC    specific in amplifying and detecting B.burgdorferi, but which distinguish
CC    other closely related species. The region from about 475 to 770 is
CC    preferred for primer and probe construction because it contains at least
CC    two small deletions in the B.hermsii sequence. (Updated on 25-MAR-2003 to
CC    correct PA field.)
XX
SQ    Sequence 1011 BP; 360 A; 175 C; 197 G; 279 T; 0 U; 0 Other;

    Query Match                100.0%;  Score 21;  DB 2;  Length 1011;
    Best Local Similarity      100.0%;  Pred. No. 13;
    Matches    21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGCAAATCTTTTCTCTGGTG 21
           |||
Db          581 TTGCAAATCTTTTCTCTGGTG 601

```

RESULT 7

SCORE Search Results Details for Application 10764186 and Search Result 20070816_164306_us-10-764-186-2.rng.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2007, 16:31:34 ; Search time 213 Seconds
(without alignments)
731.716 Million cell updates/sec

Title: US-10-764-186-2
Perfect score: 21
Sequence: 1 agaattaactccgccttgaga 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	21	100.0	21	10	ADK69888	Adk69888 Borrelia
c 2	21	100.0	381	2	AAQ41495	Aaq41495 Flagellin
c 3	21	100.0	404	2	AAQ32998	Aaq32998 DNA encod
c 4	21	100.0	747	2	AAQ41493	Aaq41493 Flagellin
c 5	21	100.0	1011	2	AAQ20720	Aaq20720 B.burgdor
c 6	21	100.0	1011	2	AAQ90744	Aaq90744 B. burgdo
c 7	21	100.0	1011	6	ABK47872	Abk47872 DNA encod
c 8	21	100.0	1011	6	ABK47871	Abk47871 DNA encod
c 9	21	100.0	1131	2	AAQ41494	Aaq41494 CKS-410 f
c 10	21	100.0	1324	2	AAQ90738	Aaq90738 B31 outer
c 11	21	100.0	1324	6	ABK47865	Abk47865 Borrelia
c 12	21	100.0	1363	2	AAQ90736	Aaq90736 B31 outer
c 13	21	100.0	1363	6	ABK47863	Abk47863 Borrelia
c 14	21	100.0	1497	2	AAQ41492	Aaq41492 CKS-776 f
c 15	21	100.0	1507	2	AAQ27078	Aaq27078 Fla gene
c 16	21	100.0	110000	2	AAX20248_07	Continuation (8 of
c 17	18.4	87.6	226	2	AAQ20449	Aaq20449 B.burgdor
c 18	18.4	87.6	1011	6	ABK47820	Abk47820 Borrelia
c 19	18.4	87.6	1011	6	ABK47874	Abk47874 DNA encod
c 20	18.4	87.6	1011	6	ABK47873	Abk47873 DNA encod
c 21	17.8	84.8	226	2	AAQ20446	Aaq20446 B.burgdor
c 22	17.8	84.8	226	2	AAQ20447	Aaq20447 B.burgdor
c 23	17.8	84.8	226	2	AAQ20448	Aaq20448 B.burgdor
c 24	17.8	84.8	504	14	AEE97083	Aee97083 Borrelia
c 25	17.8	84.8	1011	6	ABK47821	Abk47821 Borrelia
c 26	17.8	84.8	4061	14	AEE97082	Aee97082 Plasmid p
c 27	17.4	82.9	220	2	AAQ20724	Aaq20724 Specifica
c 28	17.4	82.9	220	2	AAQ20725	Aaq20725 Specifica
c 29	17.4	82.9	1005	2	AAQ20721	Aaq20721 B.harmsii
c 30	16.8	80.0	220	2	AAQ20723	Aaq20723 B.harmsii
31	16.4	78.1	2000	6	ABZ17428	Abz17428 Arabidops
32	16.2	77.1	219	11	ABD01290	Abd01290 Klebsiell
33	16.2	77.1	780	11	ABD01207	Abd01207 Klebsiell
c 34	16.2	77.1	9551	2	AAZ22301	Aaz22301 cDNA enco
c 35	16.2	77.1	20010	4	AAK73615	Aak73615 Human imm
36	16.2	77.1	23943	12	ADQ97942	Adq97942 Human can
c 37	16.2	77.1	24607	11	ACN45056	Acn45056 Mouse gen
c 38	16.2	77.1	32249	4	ABA07406	Aba07406 Human pan
c 39	16.2	77.1	32249	4	AAK91137	Aak91137 Human dig
c 40	16.2	77.1	32249	5	ABA20005	Aba20005 Human ner
c 41	16.2	77.1	42881	5	AAF97868	Aaf97868 Human neu
42	16.2	77.1	50442	4	AAK87551	Aak87551 Human imm
43	16.2	77.1	50442	4	AAK73083	Aak73083 Human imm
c 44	16.2	77.1	64482	12	ADQ59515	Adq59515 Human can
c 45	16.2	77.1	64482	14	ADZ13896	Adz13896 Murine ca

ALIGNMENTS

```

XX
DT 25-MAR-2003 (revised)
DT 20-AUG-1993 (first entry)
XX
DE Flagellin (amino acids 64-311).
XX
KW CMP-KDO synthetase; pB776; pB410; capture; immunodot; assay;
KW Treponema pallidum; syphilis;
KW CTP:CMP-3-deoxy-manno-octulosonate cytidylyl transferase; ss.
XX
OS Borrelia burgdorferi.
XX
PN WO9308208-A1.
XX
PD 29-APR-1993.
XX
PF 21-OCT-1992; 92WO-US009199.
XX
PR 21-OCT-1991; 91US-00779704.
XX
PA (ABBO ) ABBOTT LAB.
XX
PI Robinson JM, Pilot-Matias TJ, Hunt JC;
XX
DR WPI; 1993-152418/18.
DR P-PSDB; AAR36698.
XX
PT Synthetic polypeptide immuno-reactive with Borrelia Burgdorferi
PT antibodies - for diagnosis of Lyme disease.
XX
PS Claim 11; Page 42; 76pp; English.
XX
CC Expression vector pB776 encodes fusion protein CKS-776, consisting of 239
CC amino acids of CKS, 11 amino acids contributed by linker DNA sequences,
CC and amino acids 64 to 311 of B. burgdorferi flagellin. The recombinant
CC fusion proteins p776 and p410 are differentiating polypeptides which can
CC be used in capture assays and immunodot assays for the detection of B.
CC burgdorferi infection such as in Lyme disease, without false positives
CC due to Treponema pallidum infection such as in patients with syphilis.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 747 BP; 274 A; 128 C; 149 G; 196 T; 0 U; 0 Other;

Query Match          100.0%; Score 21; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches    21; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Qy      1 AGAATTAAC TCCGCCTTGAGA 21
        |||||||
Db     519 AGAATTAAC TCCGCCTTGAGA 499

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RESULT 5

AAQ20720/c

ID AAQ20720 standard; DNA; 1011 BP.

XX

AC AAQ20720;

XX

DT 25-MAR-2003 (revised)

DT 15-APR-1992 (first entry)

XX

DE B.burgdorferi flagellin gene.
 XX
 KW tick-borne spirochaete; Lyme disease; polymerase chain reaction; PCR; ss.
 XX
 OS Borrelia burgdorferi.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 390..712
 FT /*tag= b
 FT /note= "region of relative non-homology to B.hermsii"
 FT misc_feature 492..516
 FT /*tag= c
 FT /note= "primer for amplifying B.burgdorferi DNA"
 FT misc_feature 594..642
 FT /*tag= a
 FT /label= Probe
 FT /note= "specific for B.burgdorferi B31 group"
 FT misc_feature 743..767
 FT /*tag= d
 FT /note= "primer for amplifying B.burgdorferi DNA"
 XX
 PN WO9119814-A.
 XX
 PD 26-DEC-1991.
 XX
 PF 15-JUN-1990; 90US-00538957.
 XX
 PR 15-JUN-1990; 90US-00538957.
 PR 25-APR-1991; 91US-00691188.
 XX
 PA (BAXT) BAXTER DIAGNOSTICS INC.
 XX
 PI Picken RN, Ammons HC;
 XX
 DR WPI; 1992-024430/03.
 XX
 PT New DNA primers useful in diagnosis of Lyme's disease - comprise
 PT complementary strand specificity flanking Borrelia burgdorferi sequence.
 XX
 PS Disclosure; Fig 1; 47pp; English.
 XX
 CC Comparison of this sequence from B.burgdorferi with the flagellin gene of
 CC B.hermsii (see AAQ20721) revealed a region of relative non-homology. This
 CC region provides the basis for constructing primers and probes which are
 CC specific in amplifying and detecting B.burgdorferi, but which distinguish
 CC other closely related species. The region from about 475 to 770 is
 CC preferred for primer and probe construction because it contains at least
 CC two small deletions in the B.hermsii sequence. (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX
 SQ Sequence 1011 BP; 360 A; 175 C; 197 G; 279 T; 0 U; 0 Other;

 Query Match 100.0%; Score 21; DB 2; Length 1011;
 Best Local Similarity 100.0%; Pred. No. 0.91;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 AGAATTAACTCCGCCTTGAGA 21
 |||||
 Db 708 AGAATTAACTCCGCCTTGAGA 688

SCORE Search Results Details for Application 10764186 and Search Result 20070816_164306_us-10-764-186-3.rng.

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Page	List	Overview	FAQ	Suggestions

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OM nucleic - nucleic search, using sw model

Run on: August 19, 2007, 16:31:34 ; Search time 263 Seconds
(without alignments)
731.716 Million cell updates/sec

Title: US-10-764-186-3
Perfect score: 26
Sequence: 1 ccttcctgttgaaacaccctcttgaac 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	26	100.0	26	10	ADK69889	Adk69889 Borrelia
2	26	100.0	26	10	ADK69893	Adk69893 Borrelia
c 3	26	100.0	381	2	AAQ41495	Aaq41495 Flagellin
c 4	26	100.0	404	2	AAQ32998	Aaq32998 DNA encod
c 5	26	100.0	747	2	AAQ41493	Aaq41493 Flagellin
c 6	26	100.0	1011	2	AAQ20720	Aaq20720 B.burgdor
c 7	26	100.0	1011	2	AAQ90744	Aaq90744 B. burgdo
c 8	26	100.0	1011	6	ABK47872	Abk47872 DNA encod
c 9	26	100.0	1011	6	ABK47871	Abk47871 DNA encod
c 10	26	100.0	1131	2	AAQ41494	Aaq41494 CKS-410 f
c 11	26	100.0	1141	2	AAQ90737	Aaq90737 B31 outer
c 12	26	100.0	1141	6	ABK47864	Abk47864 Borrelia
c 13	26	100.0	1180	2	AAQ90735	Aaq90735 B31 outer
c 14	26	100.0	1180	6	ABK47862	Abk47862 Borrelia
c 15	26	100.0	1324	2	AAQ90738	Aaq90738 B31 outer
c 16	26	100.0	1324	6	ABK47865	Abk47865 Borrelia
c 17	26	100.0	1363	2	AAQ90736	Aaq90736 B31 outer
c 18	26	100.0	1363	6	ABK47863	Abk47863 Borrelia
c 19	26	100.0	1497	2	AAQ41492	Aaq41492 CKS-776 f
c 20	26	100.0	1507	2	AAQ27078	Aaq27078 Fla gene
c 21	26	100.0	1762	2	AAQ90739	Aaq90739 B31 Osp-A
c 22	26	100.0	1765	6	ABK47866	Abk47866 Borrelia
c 23	26	100.0	110000	2	AAX20248_07	Continuation (8 of
c 24	22.8	87.7	226	2	AAQ20447	Aaq20447 B.burgdor
c 25	21.2	81.5	226	2	AAQ20446	Aaq20446 B.burgdor
c 26	21.2	81.5	226	2	AAQ20449	Aaq20449 B.burgdor
c 27	21.2	81.5	504	14	AEE97083	Aee97083 Borrelia
c 28	21.2	81.5	641	2	AAT42465	Aat42465 Borrelia
c 29	21.2	81.5	709	2	AAT42439	Aat42439 Borrelia
c 30	21.2	81.5	1011	6	ABK47820	Abk47820 Borrelia
c 31	21.2	81.5	1011	6	ABK47874	Abk47874 DNA encod
c 32	21.2	81.5	1011	6	ABK47821	Abk47821 Borrelia
c 33	21.2	81.5	1011	6	ABK47873	Abk47873 DNA encod
c 34	21.2	81.5	4061	14	AEE97082	Aee97082 Plasmid p
c 35	19.6	75.4	226	2	AAQ20448	Aaq20448 B.burgdor
c 36	19.6	75.4	330	2	AAT42438	Aat42438 Borrelia
c 37	19.6	75.4	641	2	AAT42437	Aat42437 Borrelia
c 38	19.6	75.4	1405	15	AEH97207	Aeh97207 Human can
c 39	19.6	75.4	1601	6	ABS55969	Abs55969 Human tyr
c 40	19.2	73.8	648	8	ACA27488	Aca27488 Prokaryot
c 41	19.2	73.8	1527	8	ADA70596	Ada70596 Rice gene
c 42	19.2	73.8	1527	12	ADJ39422	Adj39422 Plant cDN
c 43	19.2	73.8	2241	6	ABV75472	Abv75472 AP-2gamma
c 44	18.6	71.5	470	6	ABI99631	Abi99631 Mouse isc
c 45	18.6	71.5	933	4	AAH31889	Aah31889 Human olf

ALIGNMENTS

Qy 1 CCTTCCTGTTGAACACCCTCTTGAAC 26
 |||||
 Db 467 CCTTCCTGTTGAACACCCTCTTGAAC 442

RESULT 6

AAQ20720/c

ID AAQ20720 standard; DNA; 1011 BP.

XX

AC AAQ20720;

XX

DT 25-MAR-2003 (revised)

DT 15-APR-1992 (first entry)

XX

DE B.burgdorferi flagellin gene.

XX

KW tick-borne spirochaete; Lyme disease; polymerase chain reaction; PCR; ss.

XX

OS Borrelia burgdorferi.

XX

Key	Location/Qualifiers
-----	---------------------

FT misc_feature	390. .712
-----------------	-----------

FT	/*tag= b
----	----------

FT	/note= "region of relative non-homology to B.hermsii"
----	---

FT misc_feature	492. .516
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FT	/*tag= c
----	----------

FT	/note= "primer for amplifying B.burgdorferi DNA"
----	--

FT misc_feature	594. .642
-----------------	-----------

FT	/*tag= a
----	----------

FT	/label= Probe
----	---------------

FT	/note= "specific for B.burgdorferi B31 group"
----	---

FT misc_feature	743. .767
-----------------	-----------

FT	/*tag= d
----	----------

FT	/note= "primer for amplifying B.burgdorferi DNA"
----	--

XX

PN WO9119814-A.

XX

PD 26-DEC-1991.

XX

PF 15-JUN-1990; 90US-00538957.

XX

PR 15-JUN-1990; 90US-00538957.

PR 25-APR-1991; 91US-00691188.

XX

PA (BAXT) BAXTER DIAGNOSTICS INC.

XX

PI Picken RN, Ammons HC;

XX

DR WPI; 1992-024430/03.

XX

PT New DNA primers useful in diagnosis of Lyme's disease - comprise

PT complementary strand specificity flanking Borrelia burgdorferi sequence.

XX

PS Disclosure; Fig 1; 47pp; English.

XX

CC Comparison of this sequence from B.burgdorferi with the flagellin gene of

CC B.hermsii (see AAQ20721) revealed a region of relative non-homology. This

CC region provides the basis for constructing primers and probes which are

CC specific in amplifying and detecting B.burgdorferi, but which distinguish

CC other closely related species. The region from about 475 to 770 is

CC preferred for primer and probe construction because it contains at least

CC two small deletions in the B.hermsii sequence. (Updated on 25-MAR-2003 to
 CC correct PA field.)

XX

SQ Sequence 1011 BP; 360 A; 175 C; 197 G; 279 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 2; Length 1011;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCCTGTTGAACACCCTCTTGAAC 26
 |||||
 Db 656 CCTTCCTGTTGAACACCCTCTTGAAC 631

RESULT 7

AAQ90744/c

ID AAQ90744 standard; DNA; 1011 BP.

XX

AC AAQ90744;

XX

DT 30-JUL-1996 (first entry)

XX

DE B. burgdorferi strain B31 antigen P41 (P41-B31) DNA.

XX

KW Strain B31; P41 antigen; antigenic domain; chimaeric protein; treatment;
 KW diagnosis; infection; vaccine; Lyme borreliosis; immunodiagnostic assay;
 KW antibody; T-cell reactivity; chimeric; ds.

XX

OS Borrelia burgdorferi.

XX

FH Key Location/Qualifiers

FT CDS 1. .1011

FT /*tag= a

XX

PN WO9512676-A1.

XX

PD 11-MAY-1995.

XX

PF 27-OCT-1994; 94WO-US012352.

XX

PR 01-NOV-1993; 93US-00148191.

PR 29-APR-1994; 94US-00235836.

XX

PA (ASUY-) ASSOC UNIVERSITIES INC.

XX

PI Dunn JJ, Luft BJ;

XX

DR WPI; 1995-215034/28.

DR P-PSDB; AAR75747.

XX

PT Chimeric protein comprising 2 or more antigenic Borrelia polypeptide(s) -
 PT useful in a vaccine against Lyme borreliosis and in immuno:diagnostic
 PT assays.

XX

PS Example 1; Fig 40; 200pp; English.

XX

CC The present sequence encodes the B. burgdorferi strain B31, antigen P41
 CC (P41-B31). Using chemical or enzymatic methods, peptide fragments of P41-
 CC B31 were prepd., and analysed by western blot to assess their ability to
 CC bind different anti-P41 monoclonal antibodies. The information obt'd. was
 CC used to locate antigenic domains in P41-B31, the epitopes of which were

SCORE Search Results Details for Application 10764186 and Search Result 20070816_164306_us-10-764-186-6.rng.

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GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2007, 16:31:34 ; Search time 263 Seconds
(without alignments)
731.716 Million cell updates/sec

Title: US-10-764-186-6
Perfect score: 26
Sequence: 1 atcatgatgttcaagttgtgttttgc 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
No.						
1	26	100.0	26	10	ADK69892	Adk69892 Human pla
2	26	100.0	26	10	ADK69894	Adk69894 Human pla
c 3	26	100.0	242	2	AAQ25434	Aaq25434 HLA Class
c 4	26	100.0	242	2	AAQ25172	Aaq25172 PCR prod.
c 5	26	100.0	242	2	AAT87089	Aat87089 HLA Class
c 6	26	100.0	249	14	AEB23391	Aeb23391 HLA-DQ al
c 7	26	100.0	434	3	AAA45351	Aaa45351 Human sec
c 8	26	100.0	440	3	AAC04158	Aac04158 Human sec
c 9	26	100.0	441	9	ACH27689	Ach27689 Human adu
c 10	26	100.0	467	9	ACH21926	Ach21926 Human adu
c 11	26	100.0	501	7	ADS71730	Ads71730 Human kid
c 12	26	100.0	501	7	ADW40584	Adw40584 cDNA elev
c 13	26	100.0	512	10	ACD95045	Acd95045 Human col
c 14	26	100.0	580	4	AAS28875	Aas28875 Human imm
c 15	26	100.0	580	4	ABA06612	Aba06612 Human cDN
c 16	26	100.0	580	6	ABV83949	Abv83949 Human pol
c 17	26	100.0	580	10	ADB31600	Adb31600 Human cDN
c 18	26	100.0	613	14	AEB23389	Aeb23389 HLA-DQ al
c 19	26	100.0	681	11	ADP65643	Adp65643 Human (cl
c 20	26	100.0	750	14	AEB23390	Aeb23390 HLA-DQ al
c 21	26	100.0	768	6	ABQ74306	Abq74306 Human leu
c 22	26	100.0	768	6	ABQ74305	Abq74305 Human leu
c 23	26	100.0	768	14	ADV43942	Adv43942 Human psy
c 24	26	100.0	768	14	AEB23385	Aeb23385 HLA-DQ al
c 25	26	100.0	768	14	AEB23388	Aeb23388 HLA-DQ al
c 26	26	100.0	768	14	AEB23386	Aeb23386 HLA-DQ al
c 27	26	100.0	768	14	AEB23383	Aeb23383 HLA-DQ al
c 28	26	100.0	768	14	AEB23384	Aeb23384 HLA-DQ al
c 29	26	100.0	768	14	AEB23387	Aeb23387 HLA-DQ al
c 30	26	100.0	995	4	ABA06355	Aba06355 Human cDN
c 31	26	100.0	995	6	ABV83692	Abv83692 Human pol
c 32	26	100.0	1020	4	AAS28832	Aas28832 Human imm
c 33	26	100.0	1020	10	ADB31557	Adb31557 Human cDN
c 34	26	100.0	1030	11	ADP65645	Adp65645 Human MHC
c 35	26	100.0	1060	2	AAQ25064	Aaq25064 Human HLA
c 36	26	100.0	1060	6	ABK64536	Abk64536 Human ben
c 37	26	100.0	1060	12	ADQ22001	Adq22001 Human sof
c 38	26	100.0	1060	12	ADQ17229	Adq17229 Human sof
c 39	26	100.0	1060	12	ADQ17273	Adq17273 Human sof
c 40	26	100.0	1096	11	ADP65079	Adp65079 Human maj
c 41	26	100.0	1096	12	ADL26813	Adl26813 Human HLA
c 42	26	100.0	1096	12	ADP10365	Adp10365 Reference
c 43	26	100.0	1096	14	ADX25963	Adx25963 Novel cel
c 44	26	100.0	1096	15	AEG19983	Aeg19983 Neuroblas
c 45	26	100.0	1116	14	AEB29690	Aeb29690 Human pho

ALIGNMENTS

Qy 1 ATCATGATGTTCAAGTTGTGTTTTGC 26
 |||||
 Db 205 ATCATGATGTTCAAGTTGTGTTTTGC 180

RESULT 5

AAT87089/c

ID AAT87089 standard; DNA; 242 BP.

XX

AC . AAT87089;

XX

DT 25-MAR-2003 (revised)

DT 07-JAN-1998 (first entry)

XX

DE HLA Class II amplification product.

XX

KW RNA; plasma; human; HLA Class II; histocompatibility;

KW polymerase chain reaction; PCR; ss.

XX

OS Homo sapiens.

XX

PN US5654179-A.

XX

PD 05-AUG-1997.

XX

PF 03-OCT-1994; 94US-00317220.

XX

PR 14-NOV-1990; 90US-00614921.

PR 19-JUN-1992; 92US-00901545.

PR 08-APR-1993; 93US-00044649.

XX

PA (HYDS) HRI RES INC.

XX

PI Lin L;

XX

DR WPI; 1997-401849/37.

XX

PT Preparation of RNA samples from plasma - by alcohol precipitation after
 PT lysis with guanidinium thiocyanate.

XX

PS Disclosure; Col 45-46; 60pp; English.

XX

CC This DNA sequence comprises a PCR amplification product of human
 CC histocompatibility (HLA) class II genes (see also AAT87090-91). It was
 CC produced from human placental DNA. A claimed method for preparing RNA
 CC samples comprises: (a) mixing plasma with an aqueous buffer solution
 CC containing guanidinium thiocyanate and beta- mercaptoethanol; (b) heating
 CC the mixture; (c) adding an equal volume of an alcohol to precipitate RNA;
 CC and (d) recovering the RNA. The method can be used to prepare RNA samples
 CC for subsequent amplification, especially for detecting pathogens, e.g.
 CC HCV or HIV. Compared with the known 'IsoQuick' and 'RNAzol' methods,
 CC the method uses fewer tubes (just one), requires fewer steps, takes less
 CC time and produces no toxic waste. (Updated on 25-MAR-2003 to correct PF
 CC field.)

XX

SQ Sequence 242 BP; 61 A; 56 C; 68 G; 57 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 2; Length 242;

Best Local Similarity 100.0%; Pred. No. 0.46;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCATGATGTTCAAGTTGTGTTTTGC 26
 |||||
 Db 205 ATCATGATGTTCAAGTTGTGTTTTGC 180

RESULT 6

AEB23391/c

ID AEB23391 standard; DNA; 249 BP.

XX

AC AEB23391;

XX

DT 22-SEP-2005 (first entry)

XX

DE HLA-DQ allele identification-related DNA sequence #9.

XX

KW HLA-DQ; human leukocyte antigen; diagnostic; SNP detection;

KW DNA detection; transplant rejection; cancer; diabetes; ds.

XX

OS Homo sapiens.

XX

PN JP2005185173-A.

XX

PD 14-JUL-2005.

XX

PF 25-DEC-2003; 2003JP-00430555.

XX

PR 25-DEC-2003; 2003JP-00430555.

XX

PA (CANO) CANON KK.

XX

PI Tsukada M;

XX

DR WPI; 2005-483347/49.

XX

PT Probe set for identifying human leukocyte antigen (HLA)-DQ allele in test
 PT substance in patients with organ transplant, cancer, diabetes, comprises
 PT probes such as DQA1.010101, DQA1.010102, or DQA1.010201.

XX

PS Example 2; Page; 27pp; Japanese.

XX

CC This invention relates to a novel probe set for identifying HLA-DQ (human
 CC leukocyte antigen-DQ) alleles in a test substance. The invention enables
 CC identification of HLA-DQ alleles in patients with organ transplant,
 CC cancer, diabetes and other multiple-factor diseases, and thus provides
 CC tailored medical treatment to individual patients. The present sequence
 CC is that of a human DNA sequence which was used during the design of the
 CC HLA-DQ probe set of the present invention.

XX

SQ Sequence 249 BP; 62 A; 59 C; 67 G; 61 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 14; Length 249;

Best Local Similarity 100.0%; Pred. No. 0.46;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCATGATGTTCAAGTTGTGTTTTGC 26
 |||||
 Db 217 ATCATGATGTTCAAGTTGTGTTTTGC 192

RESULT 7

AAA45351/c

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10/769,186

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10/764,186

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<input type="checkbox"/>	L7	(isolation or purification) near3 efficiency near5 (standard or control)	57
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<input type="checkbox"/>	L5	(co-isolation or co-purification) near3 (standard or control)	2
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10/764,186



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#9	Search VIC AND label* AND fluoresc* AND (TaqMan OR real time)	16:32:32	7
#8	Search #7 AND (flagellin OR FlaA) AND (TaqMan OR real time)	16:23:26	7
#7	Related Articles for PubMed (Select 10325354)	16:20:17	275
#3	Search #2 AND real time	16:15:32	26
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